

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kwon, Byoung Se

(ii) TITLE OF INVENTION: New Receptor and Related Products and Methods

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Barnard, Brown & Michaels
- (B) STREET: 306 East State Street, Suite 220
- (C) CITY: Ithaca
- (D) STATE: NY
- (E) COUNTRY: USA
- (F) ZIP: 14850

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/122,796
- (B) FILING DATE: 13-SEP-1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/012,269
- (B) FILING DATE: 01-FEB-1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/922,996
- (B) FILING DATE: 30-JUL-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/267,577
- (B) FILING DATE: 07-NOV-1988

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Michaels, Christopher A
- (B) REGISTRATION NUMBER: 34,390
- (C) REFERENCE/DOCKET NUMBER: KW04

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 607-273-1711
- (B) TELEFAX: 607-273-2609

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens  
(C) INDIVIDUAL ISOLATE: H4-1BB #1  
(D) DEVELOPMENTAL STAGE: Differentiated T-cell  
(G) CELL TYPE: Lymphocyte

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 41..805  
(D) OTHER INFORMATION: /codon\_start= 41

/product= "H4-1BB"

/number= 1

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 41..802  
(D) OTHER INFORMATION: /codon\_start= 41

/product= "H4-1BB"

/number= 1

*a4*  
*cont.* (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATCAGCTTT GCTAGTATCA TACCTGTGCC AGATTCATC ATG GGA AAC AGC TGT 55  
Met Gly Asn Ser Cys  
1 5

TAC AAC ATA GTA GCC ACT CTG TTG CTG GTC CTC AAC TTT GAG AGG ACA 103  
Tyr Asn Ile Val Ala Thr Leu Leu Val Leu Asn Phe Glu Arg Thr  
10 15 20

AGA TCA TTG CAG GAT CCT TGT AGT AAC TGC CCA GCT GGT ACA TTC TGT 151  
Arg Ser Leu Asp Pro Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys  
25 30 35

GAT AAT AAC AGG AAT CAG ATT TGC AGT CCC TGT CCT CCA AAT AGT TTC 199  
Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe  
40 45 50

TCC AGC GCA GGT GGA CAA AGG ACC TGT GAC ATA TGC AGG CAG TGT AAA 247  
Ser Ser Ala Gly Gln Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys  
55 60 65

GGT GTT TTC AGG ACC AGG AAG GAG TGT TCC TCC ACC AGC AAT GCA GAG 295  
Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu  
70 75 80 85

TGT GAC TGC ACT CCA GGG TTT CAC TGC CTG GGG GCA GGA TGC AGC ATG 343  
Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly Ala Gly Cys Ser Met

90

95

100

TGT GAA CAG GAT TGT AAA CAA GGT CAA GAA CTG ACA AAA AAA GGT TGT Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys 105 110 115	391
AAA GAC TGT TGC TTT GGG ACA TTT AAC GAT CAG AAA CGT GGC ATC TGT Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln Lys Arg Gly Ile Cys 120 125 130	439
CGA CCC TGG ACA AAC TGT TCT TTG GAT GGA AAG TCT GTG CTT GTG AAT Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys Ser Val Leu Val Asn 135 140 145	487
GGG ACG AAG GAG AGG GAC GTG GTC TGT GGA CCA TCT CCA GCT GAC CTC Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro Ser Pro Ala Asp Leu 150 155 160 165	535
TCT CCG GGA GCA TCC TCT GTG ACC CCG CCT GCC CCT GCG AGA GAG CCA Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala Pro Ala Arg Glu Pro 170 175 180	583
GGA CAC TCT CCG CAG ATC ATC TCC TTC TTT CTT GCG CTG ACG TCG ACT Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu Ala Leu Thr Ser Thr 185 190 195	631
GCG TTG CTC TTC CTG CTG TTC CTC ACG CTC CGT TTC TCT GTT GTT Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu Arg Phe Ser Val Val 200 205 210	679
AAA CGG GGC AGA AAG AAA CTC CTG TAT ATA TTC AAA CAA CCA TTT ATG Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met 215 220 225	727
AGA CCA GTA CAA ACT ACT CAA GAG GAA GAT GGC TGT AGC TGC CGA TTT Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe 230 235 240 245	775
CCA GAA GAA GAA GAA GGA GGA TGT GAA CTG TGAAATGGAA GTCAATAGGG Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu 250 255	825
CTGTTGGGAC TTT	838

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 255 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu  
1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro

20

25

30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys  
 35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile  
 50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser  
 65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly  
 85 90 95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu  
 100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln  
 115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys  
 130 135 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro  
 145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala  
 165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu  
 180 185 190

*al.*  
*cont.*  
 Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu  
 195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe  
 210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly  
 225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu  
 245 250 255

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTYTGYMGAA ARTAYAAYCC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTYTCSTSCA HTGGTGGACA

20

(2) INFORMATION FOR SEQ ID NO:5:

*Q4*  
*cont.* (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCARGSWRC AGGTYTTRCA

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTYTGRTCRT TRAATGTTCC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

a<sup>4</sup>  
and.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATAAGCTTT GCTAGTATCA TACCT

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR Primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTAAGATCTC TGCAGGAGAGT GTCCTGGCTC

30